

RAW SEQUENCE LISTING PATENT APPLICATION US/09/390,207

DATE: 09/21/1999
TIME: 16:08:59

Input Set: I390207.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Thomason, Arlen
2 Liu, Benxian
3 <120> TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
4 <130> FILE REFERENCE: 99-371
5 <140> CURRENT APPLICATION NUMBER: US/09/390,207
6 <141> CURRENT FILING DATE: 1999-09-07
7 <160> NUMBER OF SEQ ID NOS: 41
8 <170> SOFTWARE: PatentIn Ver. 2.0
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11 <212> TYPE: DNA
12 <213> ORGANISM: Homo sapiens
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19 acctgaggac ccgagccatt g atg gac tcg gac gag acc ggg ttc gag cac 171
20 Met Asp Ser Asp Glu Thr Gly Phe Glu His
21 1 5 10
22 tca gga ctg tgg gtt tct gtg ctg gct ggt ctt ctg ctg gga gcc tgc 219
23 Ser Gly Leu Trp Val Ser Val Leu Ala Gly Leu Leu Leu Gly Ala Cys
24 15 20 25
25 cag gca cac ccc atc cct gac tcc agt cct ctc ctg caa ttc ggg ggc 267
26 Gln Ala His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly
27 30 35 40
28 caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa 315
29 Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu
30 45 50 55
31 gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac 363
32 Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp
33 60 65 70
34 cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt 411
35 Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val
36 75 80 85 90
37 att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca 459
38 Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro
39 95 100 105
40 gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc 507
41 Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser
42 110 115 120
43 ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa 555
44 Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu

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45 125 130 135
46 gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg 603
47 Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg
48 140 145 150
49 gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg 651
50 Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu
51 155 160 165 170
52 ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc 699
53 Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro
54 175 180 185
55 gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc 747
56 Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly
57 190 195 200
58 cga agc ccc agc tac gct tcc tga agccagaggc tgtttactat gacatctcct 801
59 Arg Ser Pro Ser Tyr Ala Ser
60 205 210
61 ctttatttat taggttattt atcttattta tttttttatt tttcttactt gagataataa 861
62 agagttccag aggaggataa gaatgagcat gtgtgagtgt ctgagggaag acatggcagc 921
63 tggtttgtct cccttggccc ggacaatccc ctctacacct cccctcacgt ggtccgaggg 981
64 tcctggtctt ccaactgggcc tcactttttt cttttctttt cttttctttt ttttgagacg 1041
65 gagtctcgct ctgcactcca gccaggcca cagagcgaga ttccatctca aaaaaataaa 1101
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75 Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
76 20 25 30
77 Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
78 35 40 45
79 Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
80 50 55 60
81 Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
82 65 70 75 80
83 Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
84 85 90 95
85 Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
86 100 105 110
87 Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
88 115 120 125
89 Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
90 130 135 140
91 His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
92 145 150 155 160
93 Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
94 165 170 175

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98                195                200                205
99      Ser
100     <210> SEQ ID NO 3
101     <211> LENGTH: 649
102     <212> TYPE: DNA
103     <213> ORGANISM: Mus musculus
104     <220> FEATURE:
105     <221> NAME/KEY: CDS
106     <222> LOCATION: (1)..(630)
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109      Met Glu Trp Met Arg Ser Arg Val Gly Thr Leu Gly Leu Trp Val Arg
110          1          5          10          15
111      ctg ctg ctg gct gtc ttc ctg ctg ggg gtc tac caa gca tac ccc atc      96
112      Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln Ala Tyr Pro Ile
113          20          25          30
114      cct gac tcc agc ccc ctc ctc cag ttt ggg ggt caa gtc cgg cag agg      144
115      Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg
116          35          40          45
117      tac ctc tac aca gat gac gac caa gac act gaa gcc cac ctg gag atc      192
118      Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile
119          50          55          60
120      agg gag gat gga aca gtg gta ggc gca gca cac cgc agt cca gaa agt      240
121      Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser
122          65          70          75          80
123      ctc ctg gag ctc aaa gcc ttg aag cca ggg gtc att caa atc ctg ggt      288
124      Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly
125          85          90          95
126      gtc aaa gcc tct agg ttt ctt tgc caa cag cca gat gga gct ctc tat      336
127      Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr
128          100         105         110
129      gga tcg cct cac ttt gat cct gag gcc tgc agc ttc aga gaa ctg ctg      384
130      Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu
131          115         120         125
132      ctg gag gac ggt tac aat gtg tac cag tct gaa gcc cat ggc ctg ccc      432
133      Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro
134          130         135         140
135      ctg cgt ctg cct cag aag gac tcc cca aac cag gat gca aca tcc tgg      480
136      Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp
137          145         150         155         160
138      gga cct gtg cgc ttc ctg ccc atg cca ggc ctg ctc cac gag ccc caa      528
139      Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln
140          165         170         175
141      gac caa gca gga ttc ctg ccc cca gag ccc cca gat gtg ggc tcc tct      576
142      Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser
143          180         185         190
144      gac ccc ctg agc atg gta gag cct tta cag ggc cga agc ccc agc tat      624

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158              20                      25                      30
159      Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg
160              35                      40                      45
161      Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile
162              50                      55                      60
163      Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser
164              65                      70                      75                      80
165      Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly
166              85                      90                      95
167      Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr
168              100                     105                     110
169      Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu
170              115                     120                     125
171      Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro
172              130                     135                     140
173      Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp
174              145                     150                     155                     160
175      Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln
176              165                     170                     175
177      Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser
178              180                     185                     190
179      Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser Pro Ser Tyr
180              195                     200                     205
181      Ala Ser
182              210
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184      <211> LENGTH: 181
185      <212> TYPE: PRT
186      <213> ORGANISM: Homo sapiens
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191              20                      25                      30
192      Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser
193              35                      40                      45
194      Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln

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195           50           55           60
196   Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly
197           65           70           75           80
198   Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg
199           85           90           95
200   Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
201           100          105          110
202   Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro
203           115          120          125
204   Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro
205           130          135          140
206   Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val
207           145          150          155          160
208   Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser
209           165          170          175
210   Pro Ser Tyr Ala Ser
211           180
212 <210> SEQ ID NO 6
213 <211> LENGTH: 181
214 <212> TYPE: PRT
215 <213> ORGANISM: Mus musculus
216 <400> SEQUENCE: 6
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219   Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Gln Asp Thr Glu Ala His
220           20           25           30
221   Leu Glu Ile Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser
222           35           40           45
223   Pro Glu Ser Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln
224           50           55           60
225   Ile Leu Gly Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly
226           65           70           75           80
227   Ala Leu Tyr Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg
228           85           90           95
229   Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
230           100          105          110
231   Gly Leu Pro Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala
232           115          120          125
233   Thr Ser Trp Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His
234           130          135          140
235   Glu Pro Gln Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val
236           145          150          155          160
237   Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser
238           165          170          175
239   Pro Ser Tyr Ala Ser
240           180
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242 <211> LENGTH: 21
243 <212> TYPE: DNA
244 <213> ORGANISM: Mus musculus

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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY
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Line	? Error/Warning	Original Text
60	W Invalid/Missing Amino Acid Numbering	205 210
935	W "N" or "Xaa" used: Feature required	ggaaggaaaa aagcggccgc aacannnnnn nnn